Amendment to the Specification

1. Please amend line 26 of page 38 to line 6 of page 39 of the specification as follows:

-- The data obtained by the sequence analysis were firstly processed using the Molecular BioComputing Suite (Muller *et al.*, 2001) and Sequences 3.0 programs, and the deduced protein sequences were determined. The BLAST (Altschul *et al.*, 1990) and omniBLAST programs were used for the database searches, that is the comparison with already known sequences in the EMBL and SwissProt databases or with the *Eimeria tenella* genome project data ~~**(www.sanger.ac.uk/Projects/E tenella/)**~~. Two or more DNA or protein sequences were aligned using the BLAST 2 sequences ~~**(www.ncbi.nhn.nih.gov)**~~ (Tatusova and Madden, 1999), CLUSTALW ~~**(www.ebi.ac.uk)**~~ (Thompson *et al.*, 1994) and DIALIGN (Morgenstern et al., 1998; 1999) programs. In addition, the SignalP ~~**(www.cbs.dtu.dk/services/SignalP/)**~~ (Nielsen *et al.*, 1997) and Clone Manager 5 programs were used for identifying signal peptides and, respectively, planning clonings and restrictions and for searching for open reading frames.--

Clean Version of the above paragraph:

-- The data obtained by the sequence analysis were firstly processed using the Molecular BioComputing Suite (Muller *et al.*, 2001) and Sequences 3.0 programs, and the deduced protein sequences were determined. The BLAST (Altschul *et al.*, 1990) and omniBLAST programs were used for the database searches, that is the comparison with already known sequences in the EMBL and SwissProt databases or with the *Eimeria tenella* genome project data. Two or more DNA or protein sequences were aligned using the BLAST 2 sequences (Tatusova and Madden, 1999), CLUSTALW (Thompson *et al.*, 1994) and DIALIGN (Morgenstern et al., 1998; 1999) programs. In addition, the SignalP (Nielsen *et al.*, 1997) and Clone Manager 5 programs were used for identifying signal peptides and, respectively, planning clonings and restrictions and for searching for open reading frames.--

2. Please amend the table at line 17 of page 34 of the specification as follows:

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Primer (RT-PCR)	~~**Sequence (5'-3')**~~ **SEQ ID NO**
A17-22-up	~~**TCCTCATCCTTATCATCCTCATCCT**~~ **SEQ ID NO. 4**
A17-112-lo	~~**GTGGGGATGATGGTCGGG**~~ **SEQ ID NO. 5**
A17-f-length-64-up	~~**CAGGACCCCAAAATAAAATCAAAGGCTATCACA**~~ **SEQ ID NO. 6**
A17-f-length-1176-lo	~~**TGACCGGTGGTGTGTACTTCGTAAC**~~ **SEQ ID NO. 7**
*Et*ACTIN-up	~~**CTGTGAGAAGAACCGGGTGCTCTTC**~~ **SEQ ID NO. 8**
*Et*ACTIN-lo	~~**CGTGCGAAAATGCCGGACGAAGAG**~~ **SEQ ID NO. 9**

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Clean Version of the above table:

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Primer (RT-PCR)	**SEQ ID NO**
A17-22-up	SEQ ID NO. 4
A17-112-lo	SEQ ID NO. 5
A17-f-length-64-up	SEQ ID NO. 6
A17-f-length-1176-lo	SEQ ID NO. 7
*Et*ACTIN-up	SEQ ID NO. 8
*Et*ACTIN-lo	SEQ ID NO. 9

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3. Please amend the table at line 1 of page 35 of the specification as follows:

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Primer (RACE-PCR)	~~**Sequence (5'-3')**~~ **SEQ ID NO**
A17-22-up	~~**TCCTCATCCTTATCATCCTCATCCT**~~ **SEQ ID NO. 4**
A17-max-90-up	~~**TGAGGACTATCCTAGCCACCCTAGTCGGTTTC**~~ **SEQ ID NO. 10**

A17-max-150-up	~~GAGCACCTGAGTATCCTTCTCAGCTTGCAGTT~~ SEQ ID NO. 11
A17-112-lo	~~GTGGGGATGATGGTCGGG~~ SEQ ID NO. 5
A17-max-533-lo	~~TATGTTCATGATGATGATGGTGAGGATGATGG~~ SEQ ID NO. 12
A17-max-631-lo	~~AGGATGCGCAAAATGGTAGTCATGGTGATAAT~~ SEQ ID NO. 13

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Clean Version of the above table:

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Primer (RACE-PCR)	**SEQ ID NO**
A17-22-up	SEQ ID NO. 4
A17-max-90-up	SEQ ID NO. 10
A17-max-150-up	SEQ ID NO. 11
A17-112-lo	SEQ ID NO. 5
A17-max-533-lo	SEQ ID NO. 12
A17-max-631-lo	SEQ ID NO. 13

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4. Please amend the table at line 16 of page 37 of the specification as follows:

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5'-IRD-800 primer	~~**Sequence (5'-3')**~~ **SEQ ID NO**
pG8SAET-up	~~TAGGTGTAGGTATTGCATCTGTAACTT~~ SEQ ID NO. 14
pG8SAET-lo	~~CGATATATTCGGTCGCTGAGGCTTGCA~~ SEQ ID NO. 15
pG8SAET-seq-up-140	~~ATGATGACTTTACAAATACATACAGGG~~ SEQ ID NO. 16
A17-sequint-27-up	~~CGAGGAAGAGCAGCTTACCGACATCAACTAAG~~ SEQ ID NO. 17

A17-sequint-44-up	~~CCGACATCAACTAAGCTATTGGTCGGGAATTA~~ SEQ ID NO. 18
A17-sequint-385-lo	~~ATGAGGATAATTTGGCTGAGGATGCGGATAAT~~ SEQ ID NO. 19
A17-sequint-351-lo	~~GGATGAGGATGGAGGTGAAAGTGGTAAGTTGT~~ SEQ ID NO. 20
M13 reverse	~~CGAGAAACAGCTATGAC~~ SEQ ID NO. 21
M13 forward	~~GTAAAACGACGGCCAG~~ SEQ ID NO. 22
T7-Promotor	~~ATTATGCTGAGTGATATCCC~~ SEQ ID NO. 23
BGH reverse	~~TAGAAGGCACAGTCGAGG~~ SEQ ID NO. 24

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Clean Version of the above table:

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5'-IRD-800 primer	**SEQ ID NO**
pG8SAET-up	SEQ ID NO. 14
pG8SAET-lo	SEQ ID NO. 15
pG8SAET-seq-up-140	SEQ ID NO. 16
A17-sequint-27-up	SEQ ID NO. 17
A17-sequint-44-up	SEQ ID NO. 18
A17-sequint-385-lo	SEQ ID NO. 19
A17-sequint-351-lo	SEQ ID NO. 20
M13 reverse	SEQ ID NO. 21
M13 forward	SEQ ID NO. 22
T7-Promotor	SEQ ID NO. 23
BGH reverse	SEQ ID NO. 24